10 30 50
CACGCGTCCGCGGGCGCGGCCGGAGAACCCCGCAATCTTTGCGCCCACAAAATACACCGA

70 90 110
CGATGCCCGATCTACTTTAAGGGCTGAAACCCACGGGCCTGAGAGACTATAAGAGCGTTC

130 150 170
CCTACCGCCATGGAACAACGGGGACAGAACGCCCCGGCCGCTTCGGGGGCCCGGAAAAGG
M E Q R G Q N A P A A S G A R K R

190 210 230
CACGGCCCAGGACCCAGGGAGGCGCGGGGAGCCAGGCCTGGGCCCCGGGTCCCCAAGACC
H G P G P R E A R G A R P G P R V P K T

250 270 290
CTTGTGCTCGTTGTCGCCGCGGTCCTGCTGTTGGTCTCAGCTGAGTCTGCTCTGATCACC
L V L V V A A V L L L V S A E S A L I T

310 330 350
CAACAAGACCTAGCTCCCCAGCAGAGAGCGGCCCCACAACAAAAGAGGTCCAGCCCCTCA
Q Q D L A P Q Q R A A P Q Q K R S S P S

370 390 410
GAGGGATTGTGTCCACCTGGACACCATATCTCAGAAGACGGTAGAGATTGCATCTCCTGC
E G L C P P G H H I S E D G R D C I S C

430 450 470
AAATATGGACAGGACTATAGCACTCACTGGAATGACCTCCTTTTCTGCTTGCGCTGCACC
K Y G Q D Y S T H W N D L L F C L R C T

490 510 530
AGGTGTGATTCAGGTGAAGTGGAGCTAAGTCCCTGCACCACGACCAGAAACACAGTGTGT
R C D S G E V E L S P C T T T R N T V C

550 570 590
CAGTGCGAAGAAGGCACCTTCCGGGAAGAAGATTCTCCTGAGATGTGCCGGAAGTGCCGC
Q C E E G T F R E E D S P E M C R K C R

610 630 650
ACAGGGTGTCCCAGAGGGATGGTCAAGGTCGGTGATTGTACACCCTGGAGTGACATCGAA
T G C P R G M V K V G D C T P W S D I E

670 690 710
TGTGTCCACAAAGAATCAGGCATCATCATAGGAGTCACAGTTGCAGCCGTAGTCTTGATT
C V H K E S G I I I G V T V A A V V L I

730 750 770
GTGGCTGTGTTTGTTTGCAAGTCTTTACTGTGGAAGAAAGTCCTTCCTTACCTGAAAGGC
V A V F V C K S L L W K K V L P Y L K G

790 810 830
ATCTGCTCAGGTGGTGGTGGGGACCCTGAGCGTGTGGACAGAAGCTCACAACGACCTGGG
I C S G G G G D P E R V D R S S Q R P G

FIG.1A

```
        850                     870                     890
GCTGAGGACAATGTCCTCAATGAGATCGTGAGTATCTTGCAGCCCACCCAGGTCCCTGAG
A  E  D  N  V  L  N  E  I  V  S  I  L  Q  P  T  Q  V  P  E
        910                     930                     950
CAGGAAATGGAAGTCCAGGAGCCAGCAGAGCCAACAGGTGTCAACATGTTGTCCCCCGGG
Q  E  M  E  V  Q  E  P  A  E  P  T  G  V  N  M  L  S  P  G
        970                     990                     1010
GAGTCAGAGCATCTGCTGGAACCGGCAGAAGCTGAAAGGTCTCAGAGGAGGAGGCTGCTG
E  S  E  H  L  L  E  P  A  E  A  E  R  S  Q  R  R  R  L  L
        1030                    1050                    1070
GTTCCAGCAAATGAAGGTGATCCCACTGAGACTCTGAGACAGTGCTTCGATGACTTTGCA
V  P  A  N  E  G  D  P  T  E  T  L  R  Q  C  F  D  D  F  A
        1090                    1110                    1130
GACTTGGTGCCCTTTGACTCCTGGGAGCCGCTCATGAGGAAGTTGGGCCTCATGGACAAT
D  L  V  P  F  D  S  W  E  P  L  M  R  K  L  G  L  M  D  N
        1150                    1170                    1190
GAGATAAAGGTGGCTAAAGCTGAGGCAGCGGGCCACAGGGACACCTTGTACACGATGCTG
E  I  K  V  A  K  A  E  A  A  G  H  R  D  T  L  Y  T  M  L
        1210                    1230                    1250
ATAAAGTGGGTCAACAAAACCGGGCGAGATGCCTCTGTCCACACCCTGCTGGATGCCTTG
I  K  W  V  N  K  T  G  R  D  A  S  V  H  T  L  L  D  A  L
        1270                    1290                    1310
GAGACGCTGGGAGAGAGACTTGCCAAGCAGAAGATTGAGGACCACTTGTTGAGCTCTGGA
E  T  L  G  E  R  L  A  K  Q  K  I  E  D  H  L  L  S  S  G
        1330                    1350                    1370
AAGTTCATGTATCTAGAAGGTAATGCAGACTCTGCCATGTCCTAAGTGTGATTCTCTTCA
K  F  M  Y  L  E  G  N  A  D  S  A  M  S  *
        1390                    1410                    1430
GGAAGTGAGACCTTCCCTGGTTTACCTTTTTTCTGGAAAAAGCCCAACTGGACTCCAGTC
        1450                    1470                    1490
AGTAGGAAAGTGCCACAATTGTCACATGACCGGTACTGGAAGAAACTCTCCCATCCAACA
        1510                    1530                    1550
TCACCCAGTGGATGGAACATCCTGTAACTTTTCACTGCACTTGGCATTATTTTTATAAGC
        1570                    1590
TGAATGTGATAATAAGGACACTATGGAAAAAAAAAAAAAA
```

FIG. 1B

```
1   M-LG---------------------------IWTLLPLVL  h Fas protein
1   MGLS---------------------------TVPDLLLPL  h TNFR I Protein
1   MEQR---------------------------PRGCAAVAA  DR3 protein
1   MEQRGQNAPAASGARKRHGPGPREARGARPGPRVPKTLVL  HLYBX88XXprotein

13  TSVARLSSKSVNAQVTDINSKGLELRKTVTTVETQNLEGL  h Fas protein
14  VLLELLVGIYPSGVIGLVPHLGDREKRDSVCPQGKYIH--  h TNFR I Protein
14  ALLLVLLGARAQG--------GTRSPR-CDCA-GDF-H--  DR3 protein
41  VVAAVLLLVSAESALITQQDLAPQQRAAPQQKRSSPSEGL  HLYBX88XXprotein

53  HHDGQFCHKPCPPGERKARDCTVNGDEPDCVPCQEGKEYT  h Fas protein
52  PQNNSICCTKCHKGTYLYNDCPGPGQDTDCRECESGSFTA  h TNFR I Protein
41  KKIGLFCCRGCPAGHYLKAPCTEPCGNSTCLVCPQDTFLA  DR3 protein
81  ----------CPPGHHISED------GRDCISCKYGQDYS  HLYBX88XXprotein

93  DKAHFSSKCRRCRLCDEGHGLEVEINCTRTQNTKCRCKPN  h Fas protein
92  SENHLR-HCLSCSKCRKEMGQVEISSCTVDRDTVCGCRKN  h TNFR I Protein
81  WENHHNSECARCQACDEQASQVALENCSAVADTRCGCKPG  DR3 protein
105 THWNDLLFCLRCTRCD--SGEVELSPCTTTRNTVCQCEEG  HLYBX88XXprotein

133 FF----------CNSTV---CEHCDPCTK-----------  h Fas protein
131 QYRHYWSENLFQC-----FNCSLCLN-GTVH----LSCQE  h TNFR I Protein
121 WFVEC---QVSQCVSSSPFYCQPCLDCGALHRHTRLLCSR  DR3 protein
143 TFRE----------EDSPEMCRKC----------RTGCPR  HLYBX88XXprotein
```

FIG.2A

```
149 - - - - - - - C E H G I I - - - K E C - - - - - - - - T L T S N T K C K E - - -   h Fas protein
161 K Q N T V C T C H A G F F L R E N E C V S C S N C K K S L E C T K L C L P Q I E   h TNFR I Protein
158 R D T D C G T C L P G F Y E H G D G C V S C P T S T L G - S C P E R C A A V C G   DR3 protein
163 G M V K V G D C T P - - - W S D I E C V - - - - - - - - - - - H K E S G I I I G   HLYBX88XXprotein

168 - - - - - E G S R S N L G W - - - - - - - L C L L - L L P I P L I V - - - - - W   h Fas protein
201 N V K G T E D S G T T V L L P L V I F F G L C L L S L L F I G L M Y R Y Q R - W   h TNFR I Protein
197 W R Q - - - - - - - - M F W V Q V L L A G L V V P L L L G A T L T Y T Y R H C W   DR3 protein
189 - - - - - - V T V A A V V L I V A V F - - V C K S L L W K K V L P Y L K G I C S   HLYBX88XXprotein

190 V K R K E V Q K T C R K H R K E N Q G S H E S - - - - - - - - - - - - - - - - -   h Fas protein
240 - K S K L Y S I V C G K S T P E K E G E L E G T T T K P L A P N P S F S P T P G   h TNFR I Protein
229 - P H K P L - V T A D E A G M E A L T P P P A T H L S P L D S A H T L L A P P D   DR3 protein
221 - - - - - - G G G G D P E R V D R S S Q R P G A E D N V L N E I V S I L Q P T Q   HLYBX88XXprotein

213 - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - -   h Fas protein
279 F T P T L G F S P V P S S T F T S S S T Y T P G D - C P N F A A P R R E V A P P   h TNFR I Protein
267 S S E K I C T V Q L V G N S W T P G Y P E T Q E A L C P Q V T W S W D Q L - - P   DR3 protein
255 V P E Q E M E V Q E P A E - - - - - - P T G V N M L S P G - - - E S E H L - - -   HLYBX88XXprotein

213 - - - - - - - - - P T L N P E T V A I N L - - - S D V D L S K Y I T T I A G V M   h Fas protein
318 Y Q G A D P I L A T A L A S D P I P N P L Q K W E D S A H K P Q S L D T D D P A   h TNFR I Protein
305 S R A L G P A A A P T L S P - - - - - - - - - - E S P A G S P A M M L Q P G P Q   DR3 protein
283 - - - - - - - - - - - L E P A E A E R S Q R R R L L V P A N E G D P T E T L R Q   HLYBX88XXprotein
```

FIG.2B

```
241 TLSQV---------KGFVRKNGVNEAKIDEIKNDNVQDTA h Fas protein
358 TLYAVVENVPPLRWKEFVRRLGLSDHEIDRLELQNGRCLR h TNFR I Protein
335 -LYDVMDAVPARRWKEFVRTLGLREAEIEAVEVEIGR-FR DR3 protein
312 CFDDFADLVPFDSWEPLMRKLGLMDNEI-KVAKAEAAGHR HLYBX88XXprotein

272 EQKVQLLRNWHQLHGKKEA-YDTLIKDLKKANLCTLAEKI h Fas protein
398 EAQYSMLATWRRRTPRREATLELLGRVLRDMDLLGCLEDI h TNFR I Protein
373 DQQYEMLKRWRQQQP---AGLGAVYAALERMGLDGCVEDL DR3 protein
351 DTLYTMLIKWVNKTGR-DASVHTLLDALETLGERLAKQKI HLYBX88XXprotein

311 QTIILKDITSDSENSNFRNEIQSLV                h Fas protein
438 EEAL-------CGPAALPPAPSLLR                h TNFR I Protein
410 -------------RSRLQRGP                    DR3 protein
390 EDHLLSSGKFMYLEGN--ADSAMS                 HLYBX88XXprotein
```

FIG.2C

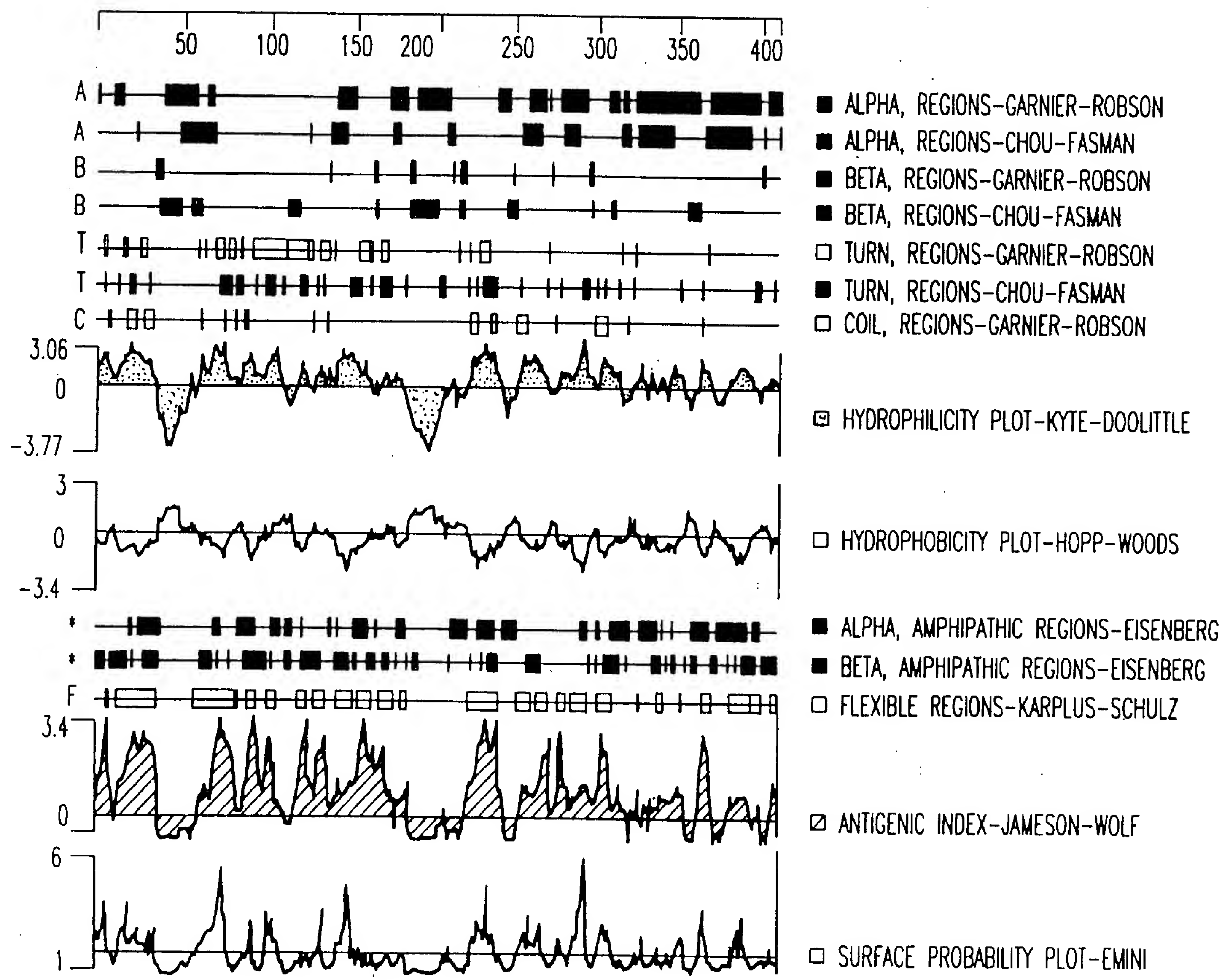

50
100
150
200
250
300
350
400
A
A
B
B
T
T
C
3.06
0
-3.77
3
0
-3.4
F
3.4
0
6
1
ALPHA, REGIONS-GARNIER-ROBSON
ALPHA, REGIONS-CHOU-FASMAN
BETA, REGIONS-GARNIER-ROBSON
BETA, REGIONS-CHOU-FASMAN
TURN, REGIONS-GARNIER-ROBSON
TURN, REGIONS-CHOU-FASMAN
COIL, REGIONS-GARNIER-ROBSON
HYDROPHILICITY PLOT-KYTE-DOOLITTLE
HYDROPHOBICITY PLOT-HOPP-WOODS
ALPHA, AMPHIPATHIC REGIONS-EISENBERG
BETA, AMPHIPATHIC REGIONS-EISENBERG
FLEXIBLE REGIONS-KARPLUS-SCHULZ
ANTIGENIC INDEX-JAMESON-WOLF
SURFACE PROBABILITY PLOT-EMINI

FIG.3

HAPBU13R

```
  1 AATTCGGCAC AGCTCTTCAG GAAGTCAGAC CTTCCCTGGT TTACCTTTTT
 51 TCTGGAAAAA GCCCAACTGG GACTCCAGTC AGTAGGAAAG TGCCACAATT
101 GTCACATGAC CGGTACTGGA AGAAACTCTC CCATCCAACA TCACCCAGTG
151 GNATGGGAAC ACTGATGAAC TTTTCACTGC ACTTGGCATT ATTTTTGTNA
201 AGCTGAATGT GATAATAAGG GCACTGATGG AAATGTCTGG ATCATTCCGG
251 TTGTGCGTAC TTTGAGATTT GNGTTTGGGG ATGTNCATTG TGTTTGACAG
301 CACTTTTTTN ATCCCTAATG TNAAATGCNT NATTTGATTG TGANTTGGGG
351 GTNAACATTG GTNAAGGNTN CCCNTNTGAC ACAGTAGNTG GTNCCCGACT
401 TANAATNGNN GAANANGATG NATNANGAAC CTTTTTTTGG GTGGGGGGGT
451 NNCGGGGCAG TNNAANGNNG NCTCCCCAGG TTTGGNGTNG CAATNGNGGA
501 ANNNTGG
```

HSBBU76R

```
  1 TTTTTTTTGT AGATGGATCT TACAATGTAG CCCAAATAAA TAAATAAAGC
 51 ATTTACATTA GGATAAAAAA GTGCTGTGAA AACAATGACA TCCCAAACCA
101 AATCTCAAAG TACGCACAAA CGGAATGATC CAGACATTTC CATAGNGTCC
151 TTATTATCAC ATTCAGCTTA TAAAANTAAT GCCAAGTGCA GTGAAAAGTT
201 ACAGGATGTT CCATCCACTG GGTGGATT
```

FIG.4

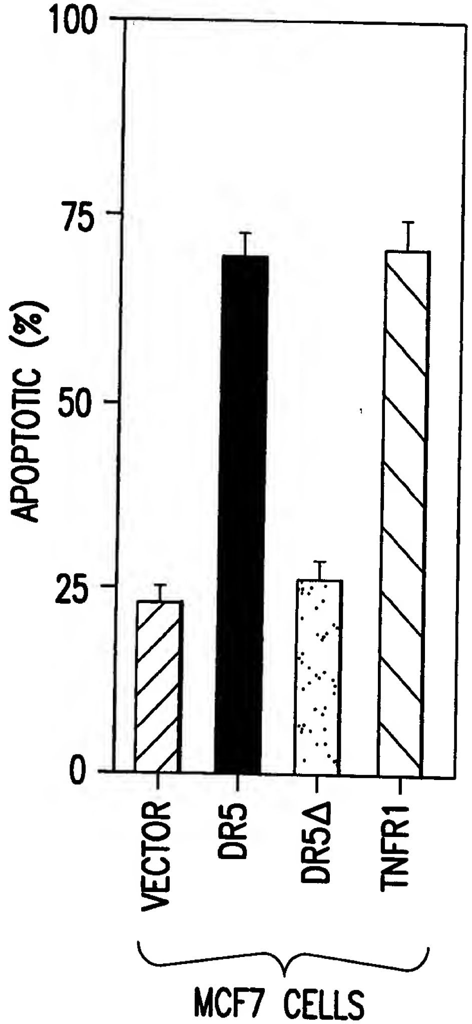


FIG. 5A

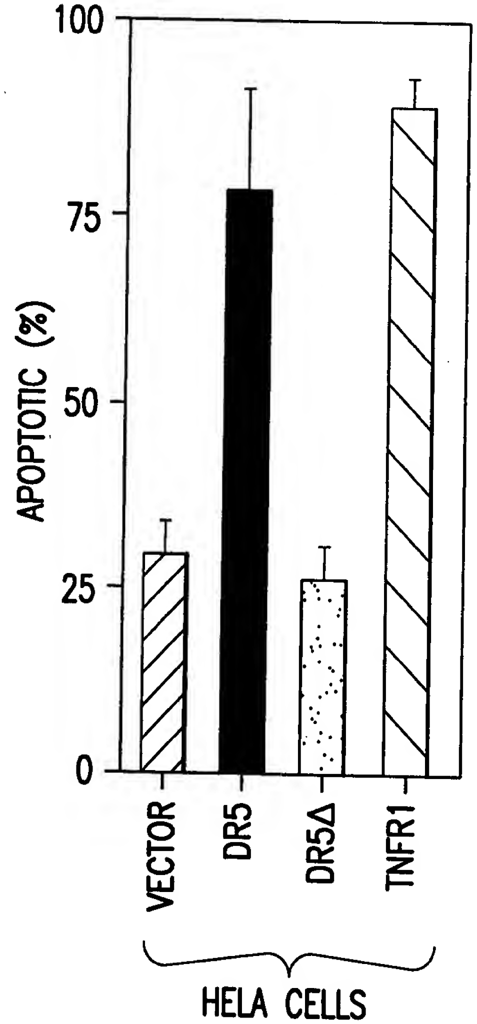


FIG. 5B

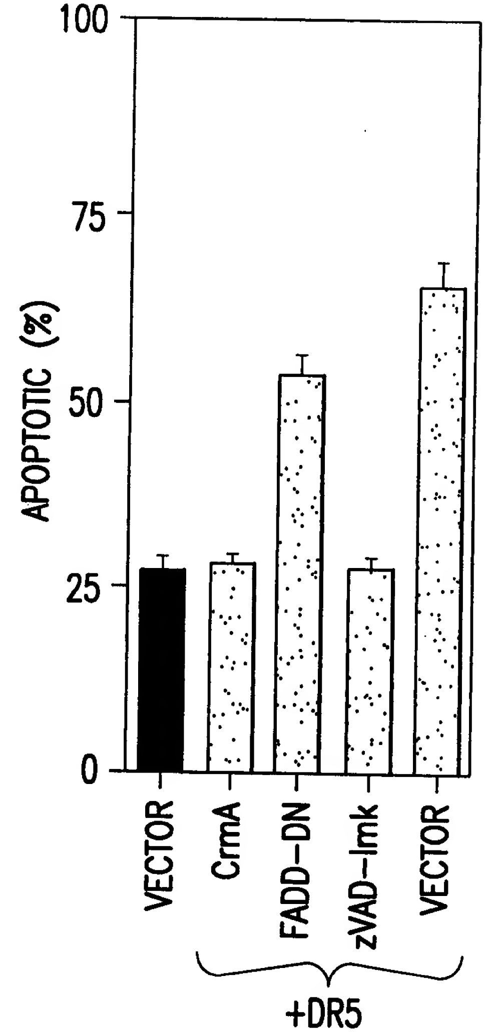
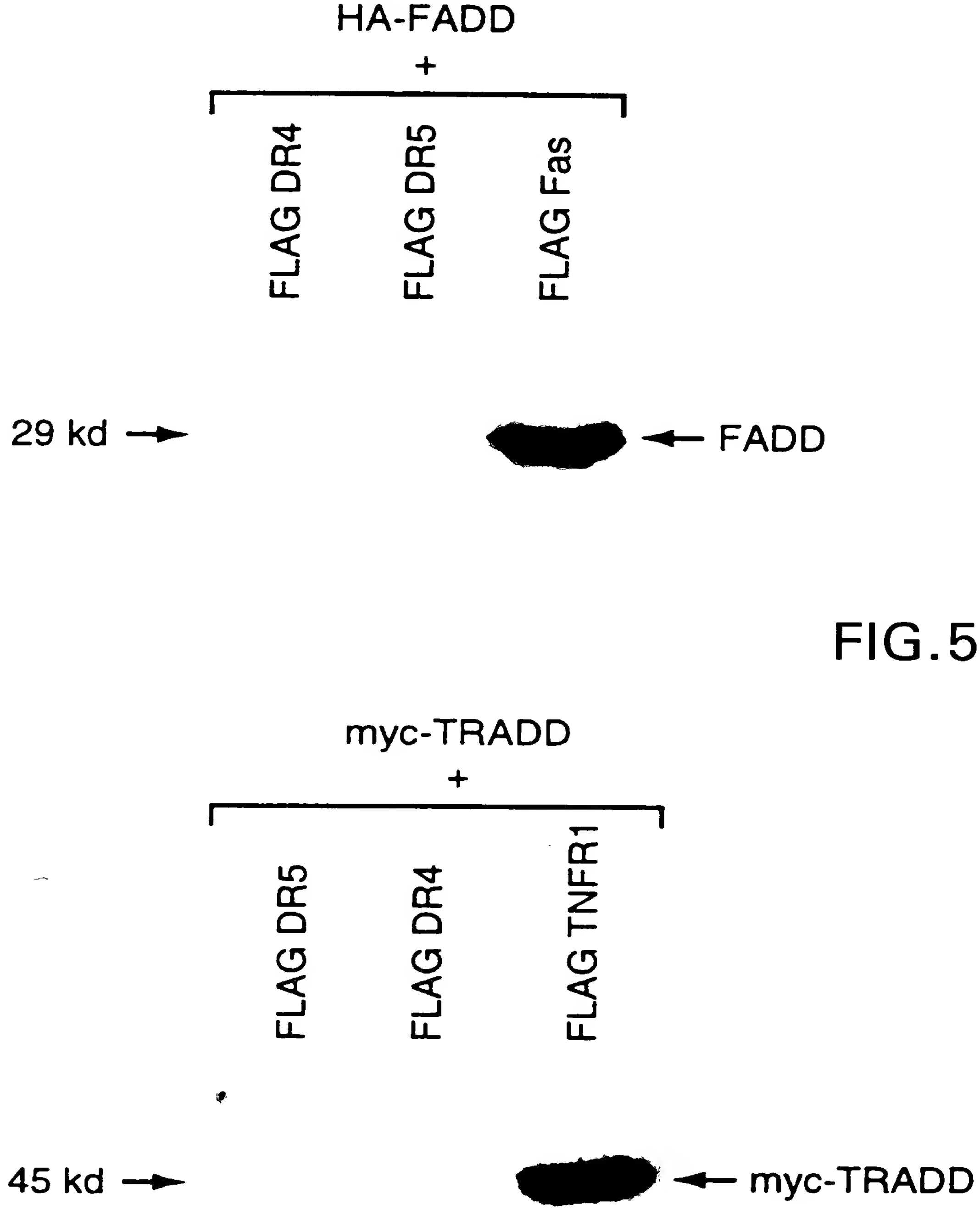


FIG. 5C



HA-FADD
+
FLAG DR4
FLAG DR5
FLAG Fas
29 kd
FADD
myc-TRADD
+
FLAG DR5
FLAG DR4
FLAG TNFR1
45 kd
myc-TRADD

FIG.5D

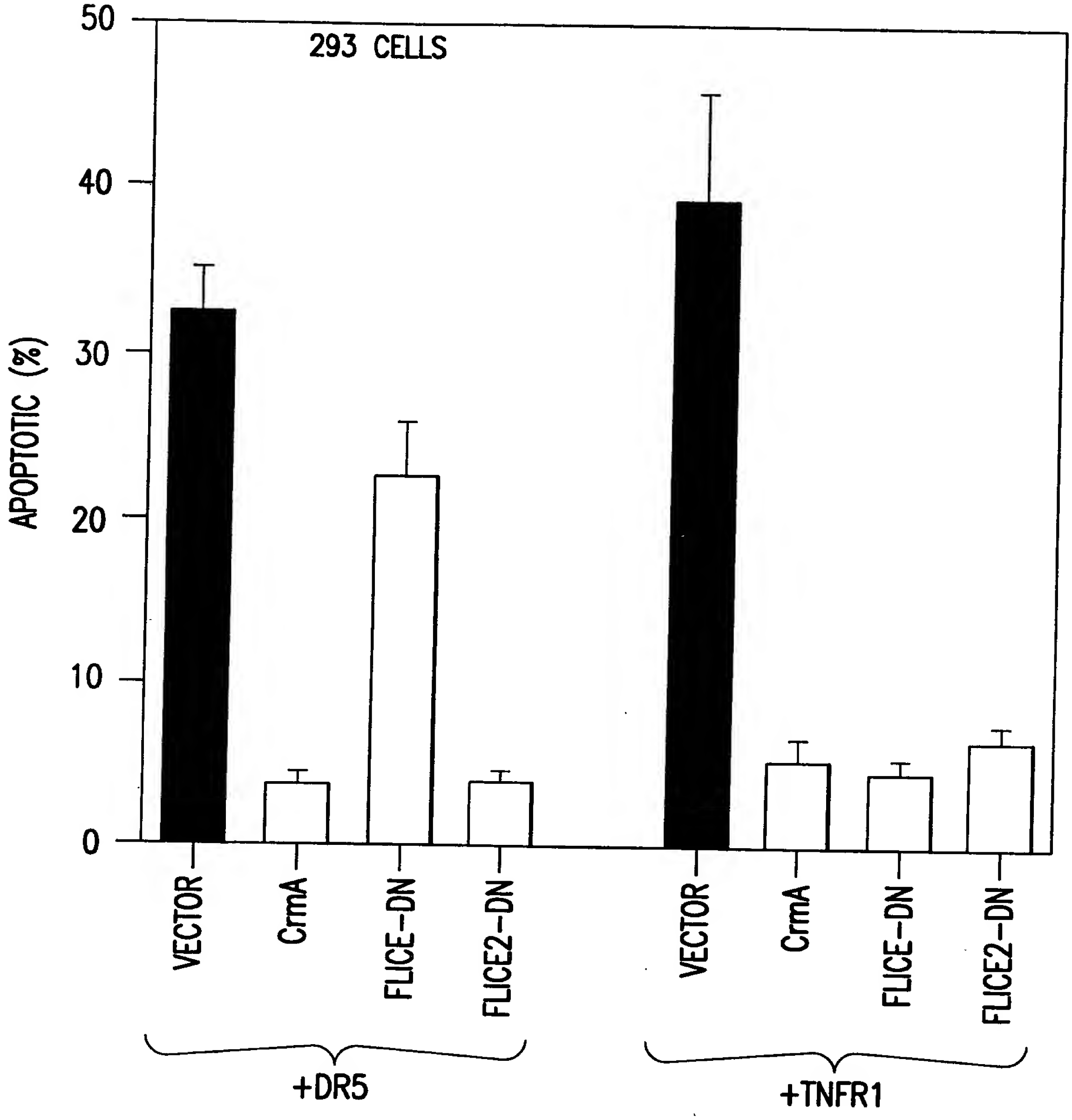

293 CELLS
APOPTOTIC (%)
50
40
30
20
10
0
VECTOR
CrmA
FLICE-DN
FLICE2-DN
VECTOR
CrmA
FLICE-DN
FLICE2-DN
+DR5
+TNFR1

FIG. 5E

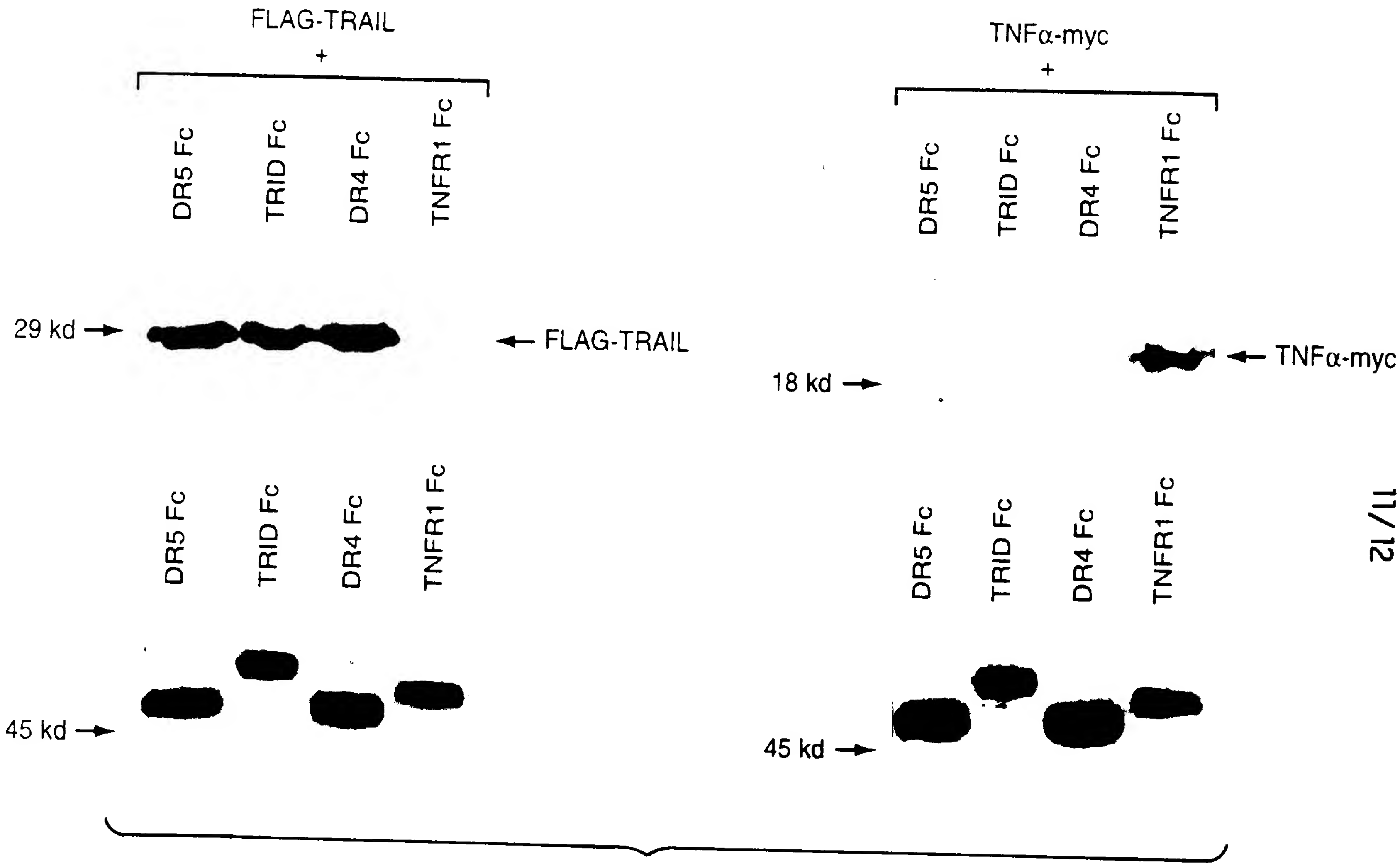

FLAG-TRAIL
+
DR5 Fc
TRID Fc
DR4 Fc
TNFR1 Fc
29 kd
FLAG-TRAIL
45 kd
TNFα-myc
+
18 kd
TNFα-myc
45 kd

FIG.6A

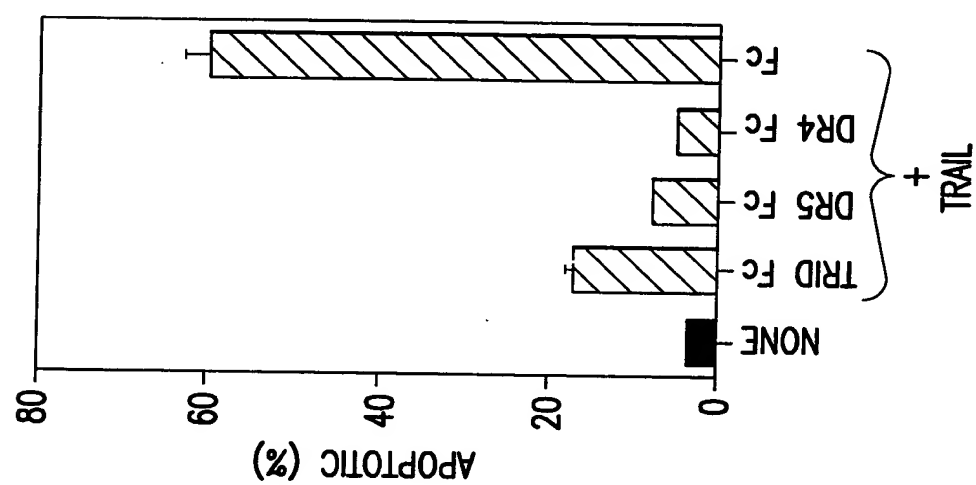

APOPTOTIC (%)
0
20
40
60
80
NONE
TRID Fc
DR5 Fc
DR4 Fc
Fc
+
TRAIL

FIG. 6B

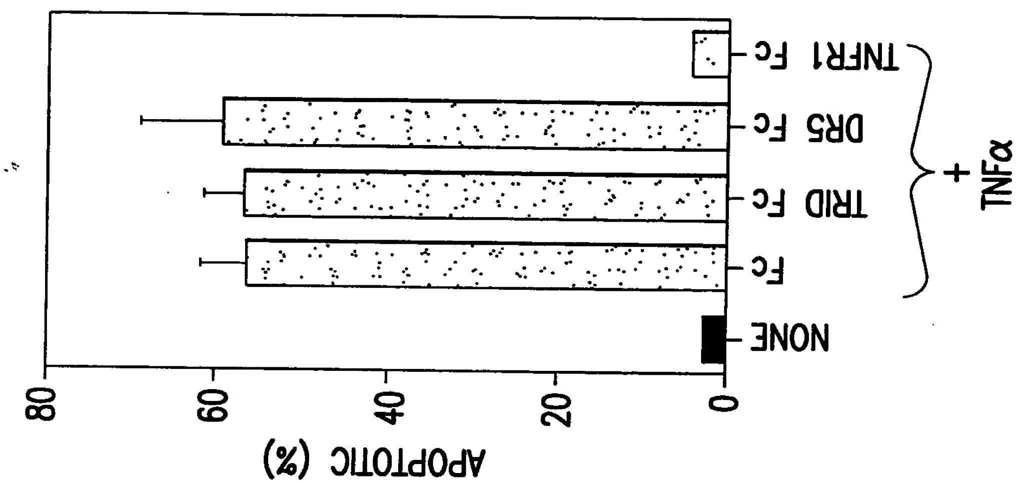

APOPTOTIC (%)
0
20
40
60
80
NONE
Fc
TRID Fc
DR5 Fc
TNFR1 Fc
+
TNFα

FIG. 6C